Blast 2 Sequences results

NCBI

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure
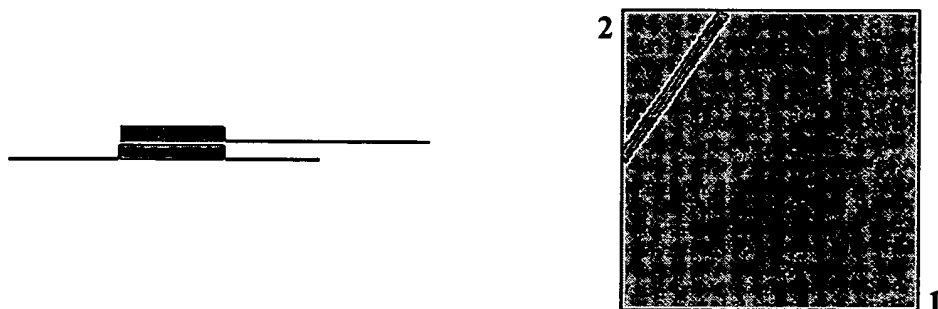
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 ☑ gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.0000 wordsize: 3 Filter ☐ View option Standard ☑

Masking character option X for protein, n for nucleotide ☑ Masking color option Black ☑

☐ Show CDS translation Align

Sequence 1: lcl|1_seq_WNV20
Length = 154 (1 .. 160)

Sequence 2: lcl|2_seq_JEV
Length = 111 (1 .. 160)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.


```
 Score = 97.8 bits (242),  Expect = 2e-19
 Identities = 42/54 (77%), Positives = 51/54 (94%), Gaps = 0/54 (0%)

Query  1    TPVGRLVTVNPFVSVATANSKVLIELEPPFSDSYIVVGRGEQQINHHWHKSGSS  54
            TPVGRLVTVNPFV+ ++ANSKVL+E+EPPF DSYIVVG G++QINHHWHK+GS+
Sbjct  58   TPVGRLVTVNPFVATSSANSKVLVEMEPPFGDSYIVVGMGDKQINHHWHKAGST  111
```

```
CPU time:      0.02 user secs.       0.00 sys. secs       0.02 total secs.

Lambda      K        H
   0.322    0.137    0.417

Gapped
Lambda      K        H
   0.267    0.0410    0.140
```

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 ▼ gap open: 11   gap extension: 1

x_dropoff: 50   expect: 10.0000 wordsize: 3   Filter ☐ View option Standard ▼

Masking character option X for protein, n for nucleotide ▼   Masking color option Black ▼

☐ Show CDS translation Align

Sequence 1: lcl|1_seq_Dengue
Length = 94 (1 .. 160)

Sequence 2: lcl|2_seq_JEV
Length = 111 (1 .. 160)
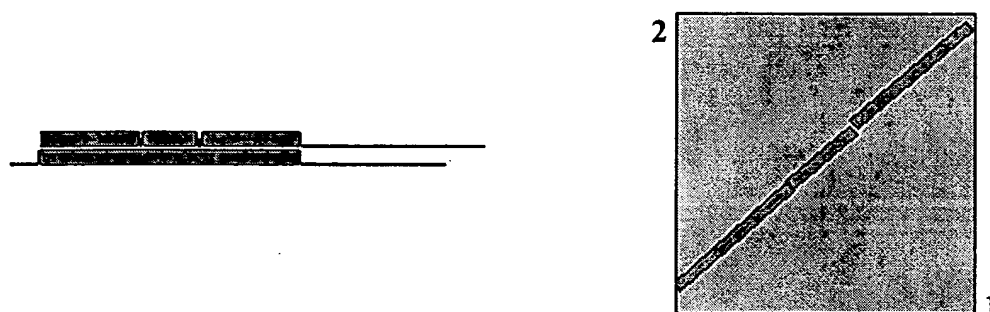
NOTE:Bitscore and expect value are calculated based on the size of the nr database.


```
 Score = 91.3 bits (225),   Expect = 1e-17
 Identities = 41/96 (42%), Positives = 61/96 (63%), Gaps = 3/96 (3%)

Query  1    MCSGKFSIDKEMAETQHGTTVVKVKYEGAGAPCKVPI-EIRDVNKEKVVGRIISSTPL--  57
            MC+ KFS   K  A+T HGT V+++ Y G+  PCK+PI  +   +N    VGR+++   P
Sbjct  12   MCTEKFSFAKNPADTGHGTVVIELSYSGSDGPCKIPIVSVASLNDMTPVGRLVTVNPFVA  71

Query  58   AENTNSVTNIELEPPFGDSYIVIGVGNSALTLHWFR  93
            + NS   +E+EPPFGDSYIV+G+G+   + HW +
Sbjct  72   TSSANSKVLVEMEPPFGDSYIVVGMGDKQINHHWHK  107


CPU time:     0.01 user secs.       0.00 sys. secs       0.01 total secs.

Lambda     K      H
   0.315   0.133   0.390
```

NCBI **Blast 2 Sequences results**

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

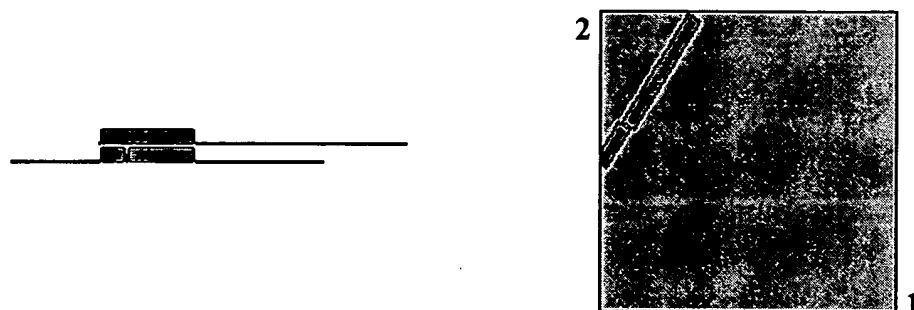## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 ⊻ gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.0000 wordsize: 3 Filter ☐ View option Standard ⊻

Masking character option X for protein, n for nucleotide ⊻ Masking color option Black ▾

☐ Show CDS translation Align

Sequence 1: lcl|1_seq_WNV20
Length = 154 (1 .. 160)

Sequence 2: lcl|2_seq_dengue
Length = 94 (1 .. 160)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.


```
 Score = 47.4 bits (111),  Expect = 2e-04
 Identities = 22/48 (45%), Positives = 28/48 (58%), Gaps = 2/48 (4%)

Query  3   VGRLVTVNPFVSVATANSKVLIELEPPFSDSYIVVGRGEQQINHHWHK  50
           VGR+++ P     NS    IELEPPF DSYIV+G G   +  HW +
Sbjct  48  VGRIISSTPLAE--NTNSVTNIELEPPFGDSYIVIGVGNSALTLHWFR  93
```

```
CPU time:     0.02 user secs.      0.00 sys. secs      0.02 total secs.

Lambda     K        H
   0.322    0.137    0.417

Gapped
Lambda     K        H
   0.267    0.0410    0.140
```

```
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 104
Number of extensions: 63
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 154
Length of database: 1,340,658,132
Length adjustment: 121
Effective length of query: 33
Effective length of database: 1,340,658,011
Effective search space: 44241714363
Effective search space used: 44241714363
Neighboring words threshold: 9
X1: 16 ( 7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.9 bits)
S2: 72 (32.3 bits)
```

Gapped
Lambda   K   H
  0.267   0.0410   0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 90
Number of extensions: 42
Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 94
Length of database: 1,357,962,904
Length adjustment: 69
Effective length of query: 25
Effective length of database: 1,357,962,835
Effective search space: 33949070875
Effective search space used: 33949070875
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (22.0 bits)
S2: 71 (32.0 bits)

```
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 135
Number of extensions: 65
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 154
Length of database: 1,340,658,132
Length adjustment: 121
Effective length of query: 33
Effective length of database: 1,340,658,011
Effective search space: 44241714363
Effective search space used: 44241714363
Neighboring words threshold: 9
X1: 16 ( 7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.9 bits)
S2: 72 (32.3 bits)
```